



SEQUENCE LISTING

<110> Prof. Dr. Werner Seeger

<120> Novel chimeric plasminogen activators and their pharmaceutical use

<130> 607927-000001

<140> US/10/583,785

<141> 2006-06-19

<160> 26

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<211> 1143

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1143)

<223> Coding sequence of the surfactant protein B precursor

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ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	

gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	

aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	

gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	

aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	

aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	

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tcc	cgg	cag	cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480
Ser	Arg	Gln	Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	
145	150	155	160	
ccc	aaa	cct	ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc	528
Pro	Lys	Pro	Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	
165	170	175		
gtc	ctc	cct	gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac	576
Val	Leu	Pro	Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	
180	185	190		
aca	cag	gat	ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc	624
Thr	Gln	Asp	Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys	
195	200	205		
tgg	ctc	tgc	agg gct ctg atc aag cgg atc caa gcc atg att ccc aag	672
Trp	Leu	Cys	Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys	
210	215	220		
ggt	gcg	cta	gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg	720
Gly	Ala	Leu	Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu	
225	230	235	240	
gtg	gcf	ggc	ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc	768
Val	Ala	Gly	Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile	
245	250	255		
ctg	ctc	gac	acg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc	816
Leu	Leu	Asp	Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg	
260	265	270		
ctc	gtc	ctc	cggtccatgatgatgacagcgtcgctggccccaaggtcgtcccg	864
Leu	Val	Leu	Arg Cys Ser Met Asp Asp Ser Ala Gly Pro Arg Ser Pro	
275	280	285		
aca	gga	gaa	tgg ctg ccg cga gac tct gag tgc cac ctc tgc atg tcc	912
Thr	Gly	Trp	Leu Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser	
290	295	300		
gtg	acc	acc	cag gcc ggg aac agc agc gag cag gcc ata cca cag gca	960
Val	Thr	Thr	Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala	
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atg	ctc	cag	gcc tgt gtt ggc tcc tgg ctg gac agg gaa aag tgc aag	1008
Met	Leu	Gln	Ala Cys Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys	
325	330	335		
caa	ttt	gtg	gag cag cac acg ccc cag ctg ctg acc ctg gtg ccc agg	1056
Gln	Phe	Val	Glu Gln His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg	
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ggc	tgg	gat	gcc cac acc acc tgc cag gcc ctc ggg gtg tgt ggg acc	1104
Gly	Trp	Asp	Ala His Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr	
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<210> 2
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (837)
 <223> Coding sequence of SP-B precursor lacking the C-terminal propeptide

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Met	Ala	Glu	Ser	His	Leu	Leu	Gln	Trp	Leu	Leu	Leu	Leu	Leu	Pro	Thr
1					5				10					15	

ctc	tgt	ggc	cca	ggc	act	gct	gcc	tgg	acc	acc	tca	tcc	ttg	gcc	tgt	96
Leu	Cys	Gly	Pro	Gly	Thr	Ala	Ala	Trp	Thr	Thr	Ser	Ser	Leu	Ala	Cys	
					20				25				30			

gcc	cag	ggc	cct	gag	ttc	tgg	tgc	caa	agc	ctg	gag	caa	gca	ttg	cag	144
Ala	Gln	Gly	Pro	Glu	Phe	Trp	Cys	Gln	Ser	Leu	Glu	Gln	Ala	Leu	Gln	
					35				40			45				

tgc	aga	gcc	cta	ggg	cat	tgc	cta	cag	gaa	gtc	tgg	gga	cat	gtg	gga	192
Cys	Arg	Ala	Leu	Gly	His	Cys	Leu	Gln	Glu	Val	Trp	Gly	His	Val	Gly	
					50				55			60				

gcc	gat	gac	cta	tgc	caa	gag	tgt	gag	gac	atc	gtc	cac	atc	ctt	aac	240
Ala	Asp	Asp	Leu	Cys	Gln	Glu	Cys	Glu	Asp	Ile	Val	His	Ile	Leu	Asn	
					65				70			75		80		

aag	atg	gcc	aag	gag	gcc	att	ttc	cag	gac	acg	atg	agg	aag	ttc	ctg	288
Lys	Met	Ala	Lys	Glu	Ala	Ile	Phe	Gln	Asp	Thr	Met	Arg	Lys	Phe	Leu	
						85			90			95				

gag	cag	gag	tgc	aac	gtc	ctc	ccc	ttg	aag	ctg	ctc	atg	ccc	cag	tgc	336
Glu	Gln	Glu	Cys	Asn	Val	Leu	Pro	Leu	Lys	Leu	Leu	Met	Pro	Gln	Cys	
					100				105			110				

aac	caa	gtg	ctt	gac	gac	tac	ttc	ccc	ctg	gtc	atc	gac	tac	ttc	cag	384
Asn	Gln	Val	Leu	Asp	Asp	Tyr	Phe	Pro	Leu	Val	Ile	Asp	Tyr	Phe	Gln	
						115			120			125				

aac	cag	act	gac	tca	aac	ggc	atc	tgt	atg	cac	ctg	ggc	ctg	tgc	aaa	432
Asn	Gln	Thr	Asp	Ser	Asn	Gly	Ile	Cys	Met	His	Leu	Gly	Leu	Cys	Lys	
						130			135			140				

tcc	cg	cag	cca	gag	cca	gag	cag	gag	cca	ggg	atg	tca	gac	ccc	ctg	480
Ser	Arg	Gln	Pro	Glu	Pro	Glu	Gln	Glu	Pro	Gly	Met	Ser	Asp	Pro	Leu	
					145				150			155		160		

ccc aaa cct ctg cg	gac cct ctg cca gac	cct ctg ctg gac aag ctc	528
Pro Lys Pro Leu Arg Asp	Pro Leu Pro Asp Pro	Leu Asp Lys Leu	
165	170	175	
gtc ctc cct gtg ctg ccc	ggg gcc ctc cag gcg agg	cct ggg cct cac	576
Val Leu Pro Val Leu Pro	Gly Ala Leu Gln Ala	Arg Pro Gly Pro His	
180	185	190	
aca cag gat ctc tcc gag	cag caa ttc ccc att	cct ctc ccc tat tgc	624
Thr Gln Asp Leu Ser Glu	Gln Gln Phe Pro Ile	Pro Leu Pro Tyr Cys	
195	200	205	
tgg ctc tgc agg gct ctg atc	aag cgg atc caa gcc atg	att ccc aag	672
Trp Leu Cys Arg Ala Leu	Ile Lys Arg Ile Gln	Ala Met Ile Pro Lys	
210	215	220	
ggt gcg cta gct gtg gca	gtg gcc cag gtg tgc	cgc gtg gta cct ctg	720
Gly Ala Leu Ala Val Ala	Val Ala Gln Val Cys	Arg Val Val Pro Leu	
225	230	235	240
gtg gcg ggc ggc atc tgc	cag tgc ctg gct gag	cgc tac tcc gtc atc	768
Val Ala Gly Gly Ile Cys	Gln Cys Leu Ala Glu	Arg Tyr Ser Val Ile	
245	250	255	
ctg ctc gac acg ctg ctg	ggc cgc atg ctg ccc	cag ctg gtc tgc cgc	816
Leu Leu Asp Thr Leu Leu	Gly Arg Met Leu Pro	Gln Leu Val Cys Arg	
260	265	270	
ctc gtc ctc cgg tgc tcc	atg		837
Leu Val Leu Arg Cys Ser	Met		
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<213> Homo sapiens

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<223> Coding sequence of the mature surfactant protein B

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cgg atc caa gcc atg att ccc aag ggt gcg cta gct gtg gca gtg gcc
Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala
20 25 30

cag gtg tgc cgc gtg gta cct ctg gtg gcg ggc ggc atc tgc cag tgc
Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys
35 40 . 45

ctg gct gag cgc tac tcc gtc atc ctg ctc gac acg ctg ctg ggc cgc	192
Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg	
50 55 60	
atg ctg ccc cag ctg gtc tgc cgc ctc gtc ctc cggtgc tcc atg	237
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gac tcc aaa ggc agc aat gaa ctt cat caa gtt cca tcg aac tgt gac	96
Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp	
20 25 30	
tgt cta aat gga gga aca tgt gtg tcc aac aag tac ttc tcc aac att	144
Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile	
35 40 45	
cac tgg tgc aac tgc cca aag aaa ttc gga ggg cag cac tgt gaa ata	192
His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile	
50 55 60	
gat aag tca aaa acc tgc tat gag ggg aat ggt cac ttt tac cga gga	240
Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly	
65 70 75 80	
aag gcc agc act gac acc atg ggc cgg ccc tgc ctg ccc tgg aac tct	288
Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser	
85 90 95	
gcc act gtc ctt cag caa acg tac cat gcc cac aga tct gat gct ctt	336
Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu	
100 105 110	
cag ctg ggc ctg ggg aaa cat aat tac tgc agg aac cca gac aac cgg	384
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg	
115 120 125	
agg cga ccc tgg tgc tat gtg cag gtg ggc cta aag ccg ctt gtc caa	432
Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln	
130 135 140	

gag tgc atg gtg cat gac tgc gca gat gga aaa aag ccc tcc tct cct			480
Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro			
145	150	155	160
cca gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc			528
Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg			
165	170	175	
ttt aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg			576
Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp			
180	185	190	
ttt gcg gcc atc tac agg agg cac cg ^g ggg ggc tct gtc acc tac gtg			624
Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val			
195	200	205	
tgt gga ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac			672
Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His			
210	215	220	
tgc ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt			720
Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly			
225	230	235	240
cgc tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg			768
Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val			
245	250	255	
gaa aac ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac			816
Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His			
260	265	270	
cac aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt			864
His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys			
275	280	285	
gcg cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat			912
Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr			
290	295	300	
aac gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa			960
Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys			
305	310	315	320
gag aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt			1008
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val			
325	330	335	
gtg aag ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc			1056
Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly			
340	345	350	
tct gaa gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa			1104
Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys			
355	360	365	

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Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu	
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Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys	
385 390 395 400	
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Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu	
405 410 415	
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Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu	
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1 5 10 15	
act ctg agg ccc cgc ttt aag att att ggg gga gaa ttc acc acc atc	96
Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile	
20 25 30	
gag aac cag ccc tgg ttt gcg gcc atc tac agg agg cac cgg ggg ggc	144
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly	
35 40 45	
tct gtc acc tac gtg tgt gga ggc agc ctc atc agc cct tgc tgg gtg	192
Ser Val Thr Tyr Val Cys Gly Ser Leu Ile Ser Pro Cys Trp Val	
50 55 60	
atc agc gcc aca cac tgc ttc att gat tac cca aag aag gag gac tac	240
Ile Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr	
65 70 75 80	
atc gtc tac ctg ggt cgc tca agg ctt aac tcc aac acg caa ggg gag	288
Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu	
85 90 95	
atg aag ttt gag gtg gaa aac ctc atc cta cac aag gac tac agc gct	336
Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala	
100 105 110	

gac acg ctt gct cac cac aac gac att gcc ttg ctg aag atc cgt tcc		384	
Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser			
115	120	125	
aag gag ggc agg tgt gcg cag cca tcc cg act ata cag acc atc tgc		432	
Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys			
130	135	140	
ctg ccc tcg atg tat aac gat ccc cag ttt ggc aca agc tgt gag atc		480	
Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile			
145	150	155	160
act ggc ttt gga aaa gag aat tct acc gac tat ctc tat ccg gag cag		528	
Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln			
165	170	175	
ctg aaa atg act gtt gtg aag ctg att tcc cac ccg gag tgt cag cag		576	
Leu Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln			
180	185	190	
ccc cac tac tac ggc tct gaa gtc acc acc aaa atg ctg tgt gct gct		624	
Pro His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala			
195	200	205	
gac cca cag tgg aaa aca gat tcc tgc cag gga gac tca ggg gga ccc		672	
Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro			
210	215	220	
ctc gtc tgt tcc ctc caa ggc cgc atg act ttg act gga att gtg agc		720	
Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser			
225	230	235	240
tgg ggc cgt gga tgt gcc ctg aag gac aag cca ggc gtc tac acg aga		768	
Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg			
245	250	255	
gtc tca cac ttc tta ccc tgg atc cgc agt cac acc aag gaa gag aat		816	
Val Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn			
260	265	270	
ggc ctg gcc ctc		828	
Gly Leu Ala Leu			
275			

<210> 6
<211> 1671
<212> DNA
<213> Artificial Sequence

<220>
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<222> (1) ... (837)
<223> Coding sequence of SP-B precursor lacking the C-terminal propeptide

<220>
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<222> (844) ... (1671)

<223> Coding sequence of low mw two-chain urokinase-plasminogen activator

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ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	96
20 25 30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	144
35 40 45	
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	192
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	240
65 70 75 80	
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	288
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	336
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	384
115 120 125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	432
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	480
145 150 155 160	
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	528
165 170 175	
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	576
180 185 190	
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys	624
195 200 205	

tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag		672	
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys			
210	215	220	
ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg		720	
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu			
225	230	235	240
gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc		768	
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile			
245	250	255	
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc		816	
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg			
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ctc gtc ctc cgg tgc tcc atg aag ctt aag ccc tcc tct cct cca gaa		864	
Leu Val Leu Arg Cys Ser Met Lys Leu Lys Pro Ser Ser Pro Pro Glu			
275	280	285	
gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag		912	
Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys			
290	295	300	
att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg		960	
Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala			
305	310	315	320
gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt gga		1008	
Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly			
325	330	335	
ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc		1056	
Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe			
340	345	350	
att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca		1104	
Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser			
355	360	365	
agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac		1152	
Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn			
370	375	380	
ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac cac aac		1200	
Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn			
385	390	395	400
gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag		1248	
Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln			
405	410	415	
cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac gat		1296	
Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp			
420	425	430	
ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat		1344	

Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn				
435	440	445		
tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag				1392
Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys				
450	455	460		
ctg att tcc cac ccg gag tgt cag cag ccc cac tac tac ggc tct gaa				1440
Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu				
465	470	475	480	
gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa aca gat				1488
Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp				
485	490	495		
tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc				1536
Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly				
500	505	510		
cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg				1584
Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu				
515	520	525		
aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg				1632
Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp				
530	535	540		
atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc				1671
Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu				
545	550	555		
<210> 7				
<211> 1674				
<212> DNA				
<213> Artificial Sequence				
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<222> (1) ... (837)				
<223> Coding sequence of SP-B precursor lacking the C-terminal propeptide				
<220>				
<221> CDS				
<222> (847) ... (1674)				
<223> Coding sequence of low mw two-chain urokinase-plasminogen activator				
<400> 7				
atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ccc acg				48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr				
1	5	10	15	
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt				96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys				
20	25	30		

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	35	40	45	144
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	50	55	60	192
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	65	70	75	240
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	85	90	95	288
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	100	105	110	336
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	115	120	125	384
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	130	135	140	432
tcc cg ^g cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	145	150	155	480
ccc aaa cct ctg cg ^g gac cct ctg cca gac cct ctg ctg gac aag ctc Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	165	170	175	528
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gc ^g agg cct ggg cct cac Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	180	185	190	576
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys	195	200	205	624
tgg ctc tgc agg gct ctg atc aag cg ^g atc caa gcc atg att ccc aag Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys	210	215	220	672
ggt gc ^g cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu	225	230	235	720
gtg gc ^g ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile	245	250	255	768
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc				816

Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	Arg	
				260				265					270			
ctc	gtc	ctc	cg	tgc	tcc	atg	cag	ata	tct	aag	ccc	tcc	tct	cct	cca	864
Leu	Val	Leu	Arg	Cys	Ser	Met	Gln	Ile	Ser	Lys	Pro	Ser	Ser	Pro	Pro	
				275				280					285			
gaa	gaa	tta	aaa	ttt	cag	tgt	ggc	caa	aag	act	ctg	agg	ccc	cgc	ttt	912
Glu	Glu	Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe	
				290				295					300			
aag	att	att	ggg	gga	gaa	ttc	acc	acc	atc	gag	aac	cag	ccc	tgg	ttt	960
Lys	Ile	Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe	
				305				310					315			320
gcg	gcc	atc	tac	agg	agg	cac	cg	ggg	ggc	tct	gtc	acc	tac	gtg	tgt	1008
Ala	Ala	Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys	
				325				330					335			
gga	ggc	agc	ctc	atc	agc	cct	tgc	tgg	gtg	atc	agc	gcc	aca	cac	tgc	1056
Gly	Gly	Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	
				340				345					350			
ttc	att	gat	tac	cca	aag	aag	gag	gac	tac	atc	gtc	tac	ctg	ggt	cgc	1104
Phe	Ile	Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg	
				355				360					365			
tca	agg	ctt	aac	tcc	aac	acg	caa	ggg	gag	atg	aag	ttt	gag	gtg	gaa	1152
Ser	Arg	Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu	
				370				375					380			
aac	ctc	atc	cta	cac	aag	gac	tac	agc	gct	gac	acg	ctt	gct	cac	cac	1200
Asn	Leu	Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	
				385				390					395			400
aac	gac	att	gcc	ttg	ctg	aag	atc	cgt	tcc	aag	gag	ggc	agg	tgt	gcg	1248
Asn	Asp	Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala	
				405				410					415			
cag	cca	tcc	cg	act	ata	cag	acc	atc	tgc	ctg	ccc	tcg	atg	tat	aac	1296
Gln	Pro	Ser	Arg	Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	Asn	
				420				425					430			
gat	ccc	cag	ttt	ggc	aca	agc	tgt	gag	atc	act	ggc	ttt	gga	aaa	gag	1344
Asp	Pro	Gln	Phe	Gly	Thr	Ser	Cys	Glu	Ile	Thr	Gly	Phe	Gly	Lys	Glu	
				435				440					445			
aat	tct	acc	gac	tat	ctc	tat	ccg	gag	cag	ctg	aaa	atg	act	gtt	gtg	1392
Asn	Ser	Thr	Asp	Tyr	Leu	Tyr	Pro	Glu	Gln	Leu	Lys	Met	Thr	Val	Val	
				450				455					460			
aag	ctg	att	tcc	cac	cg	gag	tgt	cag	cag	ccc	cac	tac	tac	ggc	tct	1440
Lys	Leu	Ile	Ser	His	Arg	Glu	Cys	Gln	Gln	Pro	His	Tyr	Tyr	Gly	Ser	
				465				470					475			480
gaa	gtc	acc	acc	aaa	atg	ctg	tgt	gct	gac	cca	cag	tgg	aaa	aca		1488
Glu	Val	Thr	Thr	Lys	Met	Leu	Cys	Ala	Ala	Asp	Pro	Gln	Trp	Lys	Thr	

485	490	495	
gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln 500	505	510	1536
ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala 515	520	525	1584
ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro 530	535	540	1632
tgg atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu 545	550	555	1674
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<211> 591			
<212> DNA			
<213> Homo sapiens			
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<221> CDS			
<222> (1) ... (591)			
<223> Coding sequence of the surfactant protein C precursor			
<400> 8			
atg gat gtg ggc agc aaa gag gtc ctg atg gag agc ccg ccg gac tac Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr 1 5 10 15			48
tcc gca gct ccc cgg ggc cga ttt ggc att ccc tgc tgc cca gtg cac Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His 20 25 30			96
ctg aaa cgc ctt ctt atc gtg gtg gtg gtg gtc ctc atc gtc gtg Leu Lys Arg Leu Leu Ile Val Val Val Val Val Leu Ile Val Val 35 40 45			144
gtg att gtg gga gcc ctg ctc atg ggt ctc cac atg agc cag aaa cac Val Ile Val Gly Ala Leu Leu Met Gly Leu His Met Ser Gln Lys His 50 55 60			192
acg gag atg gtt ctg gag atg agc att ggg gcg ccg gaa gcc cag caa Thr Glu Met Val Leu Glu Met Ser Ile Gly Ala Pro Glu Ala Gln Gln 65 70 75 80			240
cgc ctg gcc ctg agt gag cac ctg gtt acc act gcc acc ttc tcc atc Arg Leu Ala Leu Ser Glu His Leu Val Thr Thr Ala Thr Phe Ser Ile 85 90 95			288
ggc tcc act ggc ctc gtg gtg tat gac tac cag cag ctg ctg atc gcc Gly Ser Thr Gly Leu Val Val Tyr Asp Tyr Gln Gln Leu Leu Ile Ala			336

100	105	110	
tac aag cca gcc cct ggc acc tgc tgc tac atc atg aag ata gct cca Tyr Lys Pro Ala Pro Gly Thr Cys Cys Tyr Ile Met Lys Ile Ala Pro			384
115	120	125	
gag agc atc ccc agt ctt gag gct ctc act aga aaa gtc cac aac ttc Glu Ser Ile Pro Ser Leu Glu Ala Leu Thr Arg Lys Val His Asn Phe			432
130	135	140	
cag atg gaa tgc tct ctg cag gcc aag ccc gca gtg cct acg tct aag Gln Met Glu Cys Ser Leu Gln Ala Lys Pro Ala Val Pro Thr Ser Lys			480
145	150	155	160
ctg ggc cag gca gag ggg cga gat gca ggc tca gca ccc tcc gga ggg Leu Gly Gln Ala Glu Gly Arg Asp Ala Gly Ser Ala Pro Ser Gly Gly			528
165	170	175	
gac ccg gcc ttc ctg ggc atg gcc gtg agc acc ctg tgt ggc gag gtg Asp Pro Ala Phe Leu Gly Met Ala Val Ser Thr Leu Cys Gly Glu Val			576
180	185	190	
ccg ctc tac tac atc Pro Leu Tyr Tyr Ile			591
195			

<210> 9
<211> 174
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (174)
<223> Coding sequence of SP-C precursor lacking the C-terminal propeptide

atg gat gtg ggc agc aaa gag gtc ctg atg gag agc ccg ccg gac tac Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr	48
1 5 10 15	
tcc gca gct ccc cgg ggc cga ttt ggc att ccc tgc tgc cca gtg cac Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His	96
20 25 30	
ctg aaa cgc ctt ctt atc gtg gtg gtg gtg gtc ctc atc gtc gtg Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val	144
35 40 45	
gtg att gtg gga gcc ctg ctc atg ggt ctc Val Ile Val Gly Ala Leu Leu Met Gly Leu	174
50 55	

<210> 10

<211> 105
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (105)
 <223> Coding sequence of the mature surfactant protein C

<400> 10

ttt ggc att ccc tgc tgc cca	gtg cac ctg aaa cgc ctt ctt atc gtg	48
Phe Gly Ile Pro Cys Cys Pro	Val His Leu Lys Arg Leu Leu Ile Val	
1	5	10
		15
gtg gtg gtg gtg gtc ctc atc	gtc gtg gtg att gtg gga gcc ctg ctc	96
Val Val Val Val Val Leu Ile Val Val Val Ile Val Val Gly Ala Leu Leu		
20	25	30
atg ggt ctc		105
Met Gly Leu		
35		

<210> 11
 <211> 1686
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (1686)
 <223> Coding sequence of the tissue-plasminogen activator

<400> 11

atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt gga	48		
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly			
1	5	10	
		15	
gca gtc ttc gtt tcg ccc agc cag gaa atc cat gcc cga ttc aga aga	96		
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg			
20	25	30	
gga gcc aga tct tac caa gtg atc tgc aga gat gaa aaa acg cag atg	144		
Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met			
35	40	45	
ata tac cag caa cat cag tca tgg ctg cgc cct gtg ctc aga agc aac	192		
Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn			
50	55	60	
cgg gtg gaa tat tgc tgg tgc aac agt ggc agg gca cag tgc cac tca	240		
Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser			
65	70	75	80
gtg cct gtc aaa agt tgc agc gag cca agg tgt ttc aac ggg ggc acc	288		

Val	Pro	Val	Lys	Ser	Cys	Ser	Glu	Pro	Arg	Cys	Phe	Asn	Gly	Gly	Thr	
																85
																90
																95
tgc	cag	cag	gcc	ctg	tac	ttc	tca	gat	ttc	gtg	tgc	cag	tgc	ccc	gaa	336
Cys	Gln	Gln	Ala	Leu	Tyr	Phe	Ser	Asp	Phe	Val	Cys	Gln	Cys	Pro	Glu	
																100
																105
																110
gga	ttt	gct	ggg	aag	tgc	tgt	gaa	ata	gat	acc	agg	gcc	acg	tgc	tac	384
Gly	Phe	Ala	Gly	Lys	Cys	Cys	Glu	Ile	Asp	Thr	Arg	Ala	Thr	Cys	Tyr	
																115
																120
																125
gag	gac	cag	ggc	atc	agc	tac	agg	ggc	acg	tgg	agc	aca	gcg	gag	agt	432
Glu	Asp	Gln	Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Trp	Ser	Thr	Ala	Glu	Ser	
																130
																135
																140
ggc	gcc	gag	tgc	acc	aac	tgg	aac	agc	agc	gcf	ttg	gcc	cag	aag	ccc	480
Gly	Ala	Glu	Cys	Thr	Asn	Trp	Asn	Ser	Ser	Ala	Leu	Ala	Gln	Lys	Pro	
																145
																150
																160
																165
tac	agc	ggg	cgg	agg	cca	gat	gcc	atc	agg	ctg	ggc	ctg	ggg	aac	cac	528
Tyr	Ser	Gly	Arg	Arg	Pro	Asp	Ala	Ile	Arg	Leu	Gly	Leu	Gly	Asn	His	
																170
																175
																180
aac	tac	tgc	aga	aac	cca	gat	cga	gac	tca	aag	ccc	tgg	tgc	tac	gtc	576
Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Arg	Asp	Ser	Lys	Pro	Trp	Cys	Tyr	Val	
																185
																190
																195
ttt	aag	gcg	ggg	aag	tac	agc	tca	gag	ttc	tgc	agc	acc	cct	gcc	tgc	624
Phe	Lys	Ala	Gly	Lys	Tyr	Ser	Ser	Glu	Phe	Cys	Ser	Thr	Pro	Ala	Cys	
																200
																205
tct	gag	gga	aac	agt	gac	tgc	tac	ttt	ggg	aat	ggg	tca	gcc	tac	cgt	672
Ser	Glu	Gly	Asn	Ser	Asp	Cys	Tyr	Phe	Gly	Asn	Gly	Ser	Ala	Tyr	Arg	
																210
																215
																220
ggc	acg	cac	agc	ctc	acc	gag	tcg	ggt	gcc	tcc	tgc	ctc	ccg	tgg	aat	720
Gly	Thr	His	Ser	Leu	Thr	Glu	Ser	Gly	Ala	Ser	Cys	Leu	Pro	Trp	Asn	
																225
																230
																235
																240
tcc	atg	atc	ctg	ata	ggc	aag	gtt	tac	aca	gca	cag	aac	ccc	agt	gcc	768
Ser	Met	Ile	Leu	Ile	Gly	Lys	Val	Tyr	Thr	Ala	Gln	Asn	Pro	Ser	Ala	
																245
																250
																255
cag	gca	ctg	ggc	ctg	ggc	aaa	cat	aat	tac	tgc	cg	aat	cct	gat	ggg	816
Gln	Ala	Leu	Gly	Leu	Gly	Lys	His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	
																260
																265
																270
gat	gcc	aag	ccc	tgg	tgc	cac	gtg	ctg	aag	aac	cgc	agg	ctg	acg	tgg	864
Asp	Ala	Lys	Pro	Trp	Cys	His	Val	Leu	Lys	Asn	Arg	Arg	Leu	Thr	Trp	
																275
																280
																285
gag	tac	tgt	gat	gtg	ccc	tcc	tgc	tcc	acc	tgc	ggc	ctg	aga	cag	tac	912
Glu	Tyr	Cys	Asp	Val	Pro	Ser	Cys	Ser	Thr	Cys	Gly	Leu	Arg	Gln	Tyr	
																290
																295
																300
agc	cag	cct	cag	ttt	cgc	atc	aaa	gga	ggg	ctc	ttc	gcc	gac	atc	gcc	960
Ser	Gln	Pro	Gln	Phe	Arg	Ile	Lys	Gly	Gly	Leu	Phe	Ala	Asp	Ile	Ala	

305	310	315	320	
tcc cac ccc tgg cag gct gcc atc ttt gcc aag cac agg agg tcg ccc Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro				1008
325 330 335				
gga gag cggttc ctgtgc ggg ggc ata ctc atc agc tcc tgc tgg att Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile				1056
340 345 350				
ctc tct gcc gcc cac tgc ttc cag gag agg ttt ccg ccc cac cac ctg Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu				1104
355 360 365				
acg gtg atc ttg ggc aga aca tac cgg gtg gtc cct ggc gag gag gag Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu				1152
370 375 380				
cag aaa ttt gaa gtc gaa aaa tac att gtc cat aag gaa ttc gat gat Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp				1200
385 390 395 400				
gac act tac gac aat gac att gcg ctg ctg cag ctg aaa tcg gat tcg Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser				1248
405 410 415				
tcc cgc tgt gcc cag gag agc agc gtg gtc cgc act gtg tgc ctt ccc Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro				1296
420 425 430				
ccg gcg gac ctg cag ctg ccg gac tgg acg gag tgt gag ctc tcc ggc Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly				1344
435 440 445				
tac ggc aag cat gag gcc ttg tct cct ttc tat tcg gag cgg ctg aag Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys				1392
450 455 460				
gag gct cat gtc aga ctg tac cca tcc agc cgc tgc aca tca caa cat Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His				1440
465 470 475 480				
tta ctt aac aga aca gtc acc gac aac atg ctg tgt gct gga gac act Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr				1488
485 490 495				
cggtgc ggc ggg ccc cag gca aac ttg cac gac gcc tgc cag ggc gat Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp				1536
500 505 510				
tcg gga ggc ccc ctg gtgttgt ctg aac gat ggc cgc atg act ttg gtg Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val				1584
515 520 525				
ggc atc atc agc tgg ggc ctg ggc tgt gga cag aag gat gtc ccg ggt Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly				1632
530 535 540				

Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys			
85	90	95	
cgc ctc gtc ctc cggtgc tcc atg aag ccc tcc tct cct cca gaa gaa			336
Arg Leu Val Leu Arg Cys Ser Met Lys Pro Ser Ser Pro Pro Glu Glu			
100	105	110	
tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag att			384
Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile			
115	120	125	
att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg gcc			432
Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala			
130	135	140	
atc tac agg agg cac cggtgg ggc tct gtc acc tac gtg tgt gga ggc			480
Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly			
145	150	155	160
agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc att			528
Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile			
165	170	175	
gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca agg			576
Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg			
180	185	190	
ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac ctc			624
Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu			
195	200	205	
atc cta cac aag gac tac agc gct gac acg ctt gct cac cac aac gac			672
Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp			
210	215	220	
att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag cca			720
Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro			
225	230	235	240
tcc cggtatac cag acc atc tgc ctg ccc tcg atg tat aac gat ccc			768
Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro			
245	250	255	
cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat tct			816
Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser			
260	265	270	
acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag ctg			864
Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu			
275	280	285	
att tcc cac cggttgt cag cag ccc cac tac tac ggc tct gaa gtc			912
Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val			
290	295	300	
acc acc aaa atg ctg tgt gct gac cca cag tgg aaa aca gat tcc			960
Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser			

305	310	315	320	
tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc cg Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg				1008
325		330		335
atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg aag Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys				1056
340		345		350
gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg atc Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile				1104
355		360		365
cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc cat cat cat cat Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu His His His His				1152
370		375		380
cat cat				1158
His His				
				385
<210> 13				
<211> 1149				
<212> DNA				
<213> Artificial Sequence				
<220>				
<221> sig_peptide				
<222> (1) ... (60)				
<223> Signal sequence of the urokinase plasminogen activator				
<220>				
<221> CDS				
<222> (67) ... (894)				
<223> Coding sequence of low mw two-chain urokinase-plasminogen activator				
<220>				
<221> CDS				
<222> (895) ... (1131)				
<223> Coding sequence of the mature surfactant protein B				
<220>				
<221> CDS				
<222> (1132) ... (1149)				
<223> Hexahistidin affinity tag				
<400> 13				
atg aga gcc ctg ctg gcg cgc ctg ctt ctc tgc gtc ctg gtc gtg agc Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser				48
1	5	10		15
gac tcc aaa ggc agc aat aag ccc tcc tct cct cca gaa gaa tta aaa Asp Ser Lys Gly Ser Asn Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys				96
20		25		30

ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag att att ggg			144
Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly			
35	40	45	
gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg gcc atc tac			192
Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr			
50	55	60	
agg agg cac cg ^g ggg ggc tct gtc acc tac gtg tgt gga ggc agc ctc			240
Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser Leu			
65	70	75	80
atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc att gat tac			288
Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp Tyr			
85	90	95	
cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca agg ctt aac			336
Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn			
100	105	110	
tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac ctc atc cta			384
Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu			
115	120	125	
cac aag gac tac agc gct gac acg ctt gct cac cac aac gac att gcc			432
His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala			
130	135	140	
ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag cca tcc cg ^g			480
Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg			
145	150	155	160
act ata cag acc atc tgc ctg ccc tcg atg tat aac gat ccc cag ttt			528
Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe			
165	170	175	
ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat tct acc gac			576
Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp			
180	185	190	
tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag ctg att tcc			624
Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile Ser			
195	200	205	
cac cg ^g gag tgt cag cag ccc cac tac tac ggc tct gaa gtc acc acc			672
His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr			
210	215	220	
aaa atg ctg tgt gct gac cca cag tgg aaa aca gat tcc tgc cag			720
Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln			
225	230	235	240
gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc cgc atg act			768
Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr			
245	250	255	

ttg act gga att gtg agc tgg	ggc cgt gga tgt gcc ctg aag gac aag	816	
Leu Thr Gly Ile Val Ser Trp	Gly Arg Gly Cys Ala Leu Lys Asp Lys		
260	265	270	
cca ggc gtc tac acg aga gtc	tca cac ttc tta ccc tgg atc cgc agt	864	
Pro Gly Val Tyr Thr Arg Val	Ser His Phe Leu Pro Trp Ile Arg Ser		
275	280	285	
cac acc aag gaa gag aat ggc	ctg gcc ctc ttc ccc att cct ctc ccc	912	
His Thr Lys Glu Gln Asn Gly	Leu Ala Leu Phe Pro Ile Pro Leu Pro		
290	295	300	
tat tgc tgg ctc tgc agg gct	ctg atc aag cgg atc caa gcc atg att	960	
Tyr Cys Trp Leu Cys Arg Ala	Leu Ile Lys Arg Ile Gln Ala Met Ile		
305	310	315	320
ccc aag ggt gcg cta gct gtg	gca gtg gcc cag gtg tgc cgc gtg gta	1008	
Pro Lys Gly Ala Leu Ala Val	Ala Val Ala Gln Val Cys Arg Val Val		
325	330	335	
cct ctg gtg gcg ggc atc tgc	cag tgc ctg gct gag cgc tac tcc	1056	
Pro Leu Val Ala Gly Gly Ile	Cys Gln Cys Leu Ala Glu Arg Tyr Ser		
340	345	350	
gtc atc ctg ctc gac acg ctg	ctg ggc cgc atg ctg ccc cag ctg gtc	1104	
Val Ile Leu Leu Asp Thr Leu	Leu Gly Arg Met Leu Pro Gln Leu Val		
355	360	365	
tgc cgc ctc gtc ctc cgg tgc	tcc atg cat cat cat cat cat cat	1149	
Cys Arg Leu Val Leu Arg Cys	Ser Met His His His His His His		
370	375	380	

<210> 14
<211> 381
<212> PRT
<213> Homo sapiens

<220>

<221> PEPTIDE
<222> (1) ... (381)
<223> Surfactant protein B precursor

<400> 14

Met Ala Glu Ser His Leu Leu	Gln Trp Leu Leu Leu Leu Pro Thr		
1	5	10	15
Leu Cys Gly Pro Gly Thr Ala	Ala Trp Thr Thr Ser Ser Leu Ala Cys		
20	25	30	
Ala Gln Gly Pro Glu Phe Trp	Cys Gln Ser Leu Glu Gln Ala Leu Gln		
35	40	45	
Cys Arg Ala Leu Gly His Cys	Leu Gln Glu Val Trp Gly His Val Gly		
50	55	60	

Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
 65 70 75 80

Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu
 85 90 95

Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys
 100 105 110

Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln
 115 120 125

Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys
 130 135 140

Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu
 145 150 155 160

Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu
 165 170 175

Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His
 180 185 190

Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys
 195 200 205

Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys
 210 215 220

Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu
 225 230 235 240

Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile
 245 250 255

Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg
 260 265 270

Leu Val Leu Arg Cys Ser Met Asp Asp Ser Ala Gly Pro Arg Ser Pro
 275 280 285

Thr Gly Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser
 290 295 300

Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala
 305 310 315 320

Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys
 325 330 335

Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg
 340 345 350

Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr
 355 360 365

Met	Ser	Ser	Pro	Leu	Gln	Cys	Ile	His	Ser	Pro	Asp	Leu			
370					375							380			
<210>	15														
<211>	279														
<212>	PRT														
<213>	Homo sapiens														
<220>															
<221>	PEPTIDE														
<222>	(1) ... (279)														
<223>	Surfactant protein B precursor lacking the C-terminal propeptide														
<400>	15														
Met	Ala	Glu	Ser	His	Leu	Leu	Gln	Trp	Leu	Leu	Leu	Leu	Pro	Thr	
1					5				10				15		
Leu	Cys	Gly	Pro	Gly	Thr	Ala	Ala	Trp	Thr	Thr	Ser	Ser	Leu	Ala	Cys
								25					30		
Ala	Gln	Gly	Pro	Glu	Phe	Trp	Cys	Gln	Ser	Leu	Glu	Gln	Ala	Leu	Gln
							35		40			45			
Cys	Arg	Ala	Leu	Gly	His	Cys	Leu	Gln	Glu	Val	Trp	Gly	His	Val	Gly
							50		55			60			
Ala	Asp	Asp	Leu	Cys	Gln	Glu	Cys	Glu	Asp	Ile	Val	His	Ile	Leu	Asn
							65		70		75		80		
Lys	Met	Ala	Lys	Glu	Ala	Ile	Phe	Gln	Asp	Thr	Met	Arg	Lys	Phe	Leu
							85			90			95		
Glu	Gln	Glu	Cys	Asn	Val	Leu	Pro	Leu	Lys	Leu	Leu	Met	Pro	Gln	Cys
							100		105			110			
Asn	Gln	Val	Leu	Asp	Asp	Tyr	Phe	Pro	Leu	Val	Ile	Asp	Tyr	Phe	Gln
							115		120			125			
Asn	Gln	Thr	Asp	Ser	Asn	Gly	Ile	Cys	Met	His	Leu	Gly	Leu	Cys	Lys
							130		135			140			
Ser	Arg	Gln	Pro	Glu	Pro	Glu	Gln	Glu	Pro	Gly	Met	Ser	Asp	Pro	Leu
							145			155			160		
Pro	Lys	Pro	Leu	Arg	Asp	Pro	Leu	Pro	Asp	Pro	Leu	Leu	Asp	Lys	Leu
							165			170			175		
Val	Leu	Pro	Val	Leu	Pro	Gly	Ala	Leu	Gln	Ala	Arg	Pro	Gly	Pro	His
							180			185			190		
Thr	Gln	Asp	Leu	Ser	Glu	Gln	Gln	Phe	Pro	Ile	Pro	Leu	Pro	Tyr	Cys
							195			200			205		
Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro	Lys

210 215 220
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu
225 230 235 240
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile
245 250 255
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg
260 265 270
Leu Val Leu Arg Cys Ser Met
275

<210> 16
<211> 79
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1) ... (79)
<223> Mature surfactant protein B

<400> 16

Phe Pro Ile Pro Leu Pro Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys
1 5 10 15

Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala
20 25 30

Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys
35 40 45

Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg
50 55 60

Met Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met
65 70 75

<210> 17
<211> 431
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1) ... (431)
<223> Single-chain urokinase-plasminogen activator

<400> 17

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
1 5 10 15

Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
 20 25 30

Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
 35 40 45

His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
 50 55 60

Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
 65 70 75 80

Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
 85 90 95

Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
 100 105 110

Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
 115 120 125

Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
 130 135 140

Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
 145 150 155 160

Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
 165 170 175

Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp
 180 185 190

Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val
 195 200 205

Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His
 210 215 220

Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly
 225 230 235 240

Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val
 245 250 255

Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His
 260 265 270

His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys
 275 280 285

Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr
 290 295 300

Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
 305 310 315 320

Glu	Asn	Ser	Thr	Asp	Tyr	Leu	Tyr	Pro	Glu	Gln	Leu	Lys	Met	Thr	Val
325								330					335		
Val	Lys	Leu	Ile	Ser	His	Arg	Glu	Cys	Gln	Gln	Pro	His	Tyr	Tyr	Gly
340							345					350			
Ser	Glu	Val	Thr	Thr	Lys	Met	Leu	Cys	Ala	Ala	Asp	Pro	Gln	Trp	Lys
355						360					365				
Thr	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Ser	Leu
370						375					380				
Gln	Gly	Arg	Met	Thr	Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Arg	Gly	Cys
385					390				395			400			
Ala	Leu	Lys	Asp	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser	His	Phe	Leu
					405			410					415		
Pro	Trp	Ile	Arg	Ser	His	Thr	Lys	Glu	Gln	Asn	Gly	Leu	Ala	Leu	
					420			425				430			

<210> 18
<211> 276
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1) ... (276)
<223> Low molecular weight two-chain urokinase-plasminogen activator

<400> 18

Lys	Pro	Ser	Ser	Pro	Pro	Glu	Glu	Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys
1				5				10					15		

Thr	Leu	Arg	Pro	Arg	Phe	Lys	Ile	Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile
						20		25					30		

Glu	Asn	Gln	Pro	Trp	Phe	Ala	Ala	Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly
						35		40				45			

Ser	Val	Thr	Tyr	Val	Cys	Gly	Gly	Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val
						50		55			60				

Ile	Ser	Ala	Thr	His	Cys	Phe	Ile	Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr
65						70			75				80		

Ile	Val	Tyr	Leu	Gly	Arg	Ser	Arg	Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu
						85		90				95			

Met	Lys	Phe	Glu	Val	Glu	Asn	Leu	Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala
							100		105			110			

Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser

115	120	125
Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys		
130	135	140
Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile		
145	150	155
Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln		
165	170	175
Leu Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln		
180	185	190
Pro His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala		
195	200	205
Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro		
210	215	220
Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser		
225	230	235
Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg		
245	250	255
Val Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn		
260	265	270
Gly Leu Ala Leu		
275		

<210> 19

<211> 557

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1) ... (279)

<223> Surfactant protein B precursor lacking the C-terminal propeptide

<220>

<221> PEPTIDE

<222> (282) ... (577)

<223> Low molecular weight two-chain urokinase-plasminogen activator

<400> 19

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr		
1	5	10
		15

Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys		
20	25	30

Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln

35	40	45
Cys Arg Ala Leu Gly His Cys	Leu Gln Glu Val Trp Gly His Val Gly	
50	55	60
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn		
65	70	75
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu		
85	90	95
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys		
100	105	110
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln		
115	120	125
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys		
130	135	140
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu		
145	150	155
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu		
165	170	175
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His		
180	185	190
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys		
195	200	205
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys		
210	215	220
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu		
225	230	235
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile		
245	250	255
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg		
260	265	270
Leu Val Leu Arg Cys Ser Met Lys Leu Lys Pro Ser Ser Pro Pro Glu		
275	280	285
Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys		
290	295	300
Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala		
305	310	315
Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly		
325	330	335
Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe		

340	345	350	
Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser			
355	360	365	
Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn			
370	375	380	
Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn			
385	390	395	400
Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln			
405	410	415	
Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp			
420	425	430	
Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn			
435	440	445	
Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys			
450	455	460	
Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu			
465	470	475	480
Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp			
485	490	495	
Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly			
500	505	510	
Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu			
515	520	525	
Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp			
530	535	540	
Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu			
545	550	555	

<210> 20
 <211> 558
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> PEPTIDE
 <222> (1) ... (279)
 <223> Surfactant protein B precursor lacking the C-terminal propeptide

<220>
 <221> PEPTIDE
 <222> (283) ... (558)
 <223> Low molecular weight two-chain urokinase-plasminogen activator

<400> 20

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr
1 5 10 15

Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys
20 25 30

Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
35 40 45

Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly
50 55 60

Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
65 70 75 80

Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu
85 90 95

Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys
100 105 110

Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln
115 120 125

Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys
130 135 140

Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu
145 150 155 160

Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu
165 170 175

Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His
180 185 190

Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys
195 200 205

Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys
210 215 220

Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu
225 230 235 240

Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile
245 250 255

Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg
260 265 270

Leu Val Leu Arg Cys Ser Met Gln Ile Ser Lys Pro Ser Ser Pro Pro
275 280 285

Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe

290	295	300
Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe		
305	310	315
Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys		
325	330	335
Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys		
340	345	350
Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg		
355	360	365
Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu		
370	375	380
Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His		
385	390	395
400		
Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala		
405	410	415
Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn		
420	425	430
Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu		
435	440	445
Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val		
450	455	460
Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser		
465	470	475
480		
Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr		
485	490	495
Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln		
500	505	510
Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala		
515	520	525
Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro		
530	535	540
Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu		
545	550	555

<210> 21
<211> 197
<212> PRT
<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (197)

<223> Surfactant protein C precursor

<400> 21

Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr
1 5 10 15

Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His
20 25 30

Leu Lys Arg Leu Leu Ile Val Val Val Val Val Leu Ile Val Val
35 40 45

Val Ile Val Gly Ala Leu Leu Met Gly Leu His Met Ser Gln Lys His
50 55 60

Thr Glu Met Val Leu Glu Met Ser Ile Gly Ala Pro Glu Ala Gln Gln
65 70 75 80

Arg Leu Ala Leu Ser Glu His Leu Val Thr Thr Ala Thr Phe Ser Ile
85 90 95

Gly Ser Thr Gly Leu Val Val Tyr Asp Tyr Gln Gln Leu Leu Ile Ala
100 105 110

Tyr Lys Pro Ala Pro Gly Thr Cys Cys Tyr Ile Met Lys Ile Ala Pro
115 120 125

Glu Ser Ile Pro Ser Leu Glu Ala Leu Thr Arg Lys Val His Asn Phe
130 135 140

Gln Met Glu Cys Ser Leu Gln Ala Lys Pro Ala Val Pro Thr Ser Lys
145 150 155 160

Leu Gly Gln Ala Glu Gly Arg Asp Ala Gly Ser Ala Pro Ser Gly Gly
165 170 175

Asp Pro Ala Phe Leu Gly Met Ala Val Ser Thr Leu Cys Gly Glu Val
180 185 190

Pro Leu Tyr Tyr Ile
195

<210> 22

<211> 58

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (58)

<223> Surfactant protein C precursor lacking the C-terminal propeptide

<400> 22

Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr
1 5 10 15

Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His
20 25 30

Leu Lys Arg Leu Leu Ile Val Val Val Val Val Leu Ile Val Val
35 40 45

Val Ile Val Gly Ala Leu Leu Met Gly Leu
50 55

<210> 23
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1) ... (35)
<223> Mature surfactant protein C

<400> 23

Phe Gly Ile Pro Cys Cys Pro Val His Leu Lys Arg Leu Leu Ile Val
1 5 10 15

Val Val Val Val Val Leu Ile Val Val Val Ile Val Gly Ala Leu Leu
20 25 30

Met Gly Leu
35

<210> 24
<211> 562
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1) ... (562)
<223> Tissue-plasminogen activator

<400> 24

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15

Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg
20 25 30

Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met
35 40 45

Ile	Tyr	Gln	Gln	His	Gln	Ser	Trp	Leu	Arg	Pro	Val	Leu	Arg	Ser	Asn
50							55					60			
Arg	Val	Glu	Tyr	Cys	Trp	Cys	Asn	Ser	Gly	Arg	Ala	Gln	Cys	His	Ser
65							70					75			80
Val	Pro	Val	Lys	Ser	Cys	Ser	Glu	Pro	Arg	Cys	Phe	Asn	Gly	Gly	Thr
							85					90			95
Cys	Gln	Gln	Ala	Leu	Tyr	Phe	Ser	Asp	Phe	Val	Cys	Gln	Cys	Pro	Glu
							100					105			110
Gly	Phe	Ala	Gly	Lys	Cys	Cys	Glu	Ile	Asp	Thr	Arg	Ala	Thr	Cys	Tyr
							115					120			125
Glu	Asp	Gln	Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Trp	Ser	Thr	Ala	Glu	Ser
							130					135			140
Gly	Ala	Glu	Cys	Thr	Asn	Trp	Asn	Ser	Ser	Ala	Leu	Ala	Gln	Lys	Pro
							145					150			160
Tyr	Ser	Gly	Arg	Arg	Pro	Asp	Ala	Ile	Arg	Leu	Gly	Leu	Gly	Asn	His
							165					170			175
Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Arg	Asp	Ser	Lys	Pro	Trp	Cys	Tyr	Val
							180					185			190
Phe	Lys	Ala	Gly	Lys	Tyr	Ser	Ser	Glu	Phe	Cys	Ser	Thr	Pro	Ala	Cys
							195					200			205
Ser	Glu	Gly	Asn	Ser	Asp	Cys	Tyr	Phe	Gly	Asn	Gly	Ser	Ala	Tyr	Arg
							210					215			220
Gly	Thr	His	Ser	Leu	Thr	Glu	Ser	Gly	Ala	Ser	Cys	Leu	Pro	Trp	Asn
							225					230			240
Ser	Met	Ile	Leu	Ile	Gly	Lys	Val	Tyr	Thr	Ala	Gln	Asn	Pro	Ser	Ala
							245					250			255
Gln	Ala	Leu	Gly	Leu	Gly	Lys	His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly
							260					265			270
Asp	Ala	Lys	Pro	Trp	Cys	His	Val	Leu	Lys	Asn	Arg	Arg	Leu	Thr	Trp
							275					280			285
Glu	Tyr	Cys	Asp	Val	Pro	Ser	Cys	Ser	Thr	Cys	Gly	Leu	Arg	Gln	Tyr
							290					295			300
Ser	Gln	Pro	Gln	Phe	Arg	Ile	Lys	Gly	Gly	Leu	Phe	Ala	Asp	Ile	Ala
							305					310			320
Ser	His	Pro	Trp	Gln	Ala	Ala	Ile	Phe	Ala	Lys	His	Arg	Arg	Ser	Pro
							325					330			335
Gly	Glu	Arg	Phe	Leu	Cys	Gly	Gly	Ile	Leu	Ile	Ser	Ser	Cys	Trp	Ile
							340					345			350

Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu
355 360 365

Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu
370 375 380

Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp
385 390 395 400

Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser
405 410 415

Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro
420 425 430

Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly
435 440 445

Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys
450 455 460

Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His
465 470 475 480

Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr
485 490 495

Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp
500 505 510

Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val
515 520 525

Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly
530 535 540

Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met
545 550 555 560

Arg Pro

<210> 25
<211> 386
<212> PRT
<213> Artificial Sequence

<220>
<221> SIGNAL
<222> (1) ... (23)
<223> Signal sequence of the surfactant protein B

<220>
<221> PEPTIDE
<222> (26) ... (104)
<223> Mature surfactant protein B

<220>
<221> PEPTIDE
<222> (105) ... (380)
<223> Low molecular weight two-chain urokinase-plasminogen activator

<220>
<221> PEPTIDE
<222> (381) ... (386)
<223> Hexahistidin affinity tag

<400> 25

Met	Ala	Glu	Ser	His	Leu	Leu	Gln	Trp	Leu	Leu	Leu	Leu	Leu	Pro	Thr
1					5				10					15	
Leu	Cys	Gly	Pro	Gly	Thr	Ala	Ala	Trp	Phe	Pro	Ile	Pro	Leu	Pro	Tyr
					20			25					30		
Cys	Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro
				35			40				45				
Lys	Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro
					50		55			60					
Leu	Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val
					65		70		75		80				
Ile	Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys
				85			90				95				
Arg	Leu	Val	Leu	Arg	Cys	Ser	Met	Lys	Pro	Ser	Ser	Pro	Pro	Glu	Glu
				100			105			110					
Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe	Lys	Ile
					115		120			125					
Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe	Ala	Ala
					130		135		140						
Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys	Gly	Gly
					145		150		155		160				
Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	Phe	Ile
					165			170			175				
Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg	Ser	Arg
					180		185			190					
Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu	Asn	Leu
					195		200			205					
Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	Asn	Asp
					210		215		220						
Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro
					225		230		235		240				

Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro
245 250 255

Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser
260 265 270

Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu
275 280 285

Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val
290 295 300

Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser
305 310 315 320

Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg
325 330 335

Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys
340 345 350

Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile
355 360 365

Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu His His His His
370 375 380

His His
385

<210> 26

<211> 383

<212> PRT

<213> Artificial Sequence

<220>

<221> SIGNAL

<222> (1) ... (20)

<223> Signal sequence of the urokinase plasminogen activator

<220>

<221> PEPTIDE

<222> (23) ... (298)

<223> Low molecular weight two-chain urokinase-plasminogen activator

<220>

<221> PEPTIDE

<222> (299) ... (377)

<223> Coding sequence of the mature surfactant protein B

<220>

<221> PEPTIDE

<222> (378) ... (383)

<223> Hexahistidin affinity tag

<400> 26

Met	Arg	Ala	Leu	Leu	Ala	Arg	Leu	Leu	Leu	Cys	Val	Leu	Val	Val	Ser
1															15
Asp	Ser	Lys	Gly	Ser	Asn	Lys	Pro	Ser	Ser	Pro	Pro	Glu	Glu	Leu	Lys
															30
Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe	Lys	Ile	Ile	Gly
															45
Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe	Ala	Ala	Ile	Tyr
															60
Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys	Gly	Gly	Ser	Leu
															80
Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	Phe	Ile	Asp	Tyr
															95
Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg	Ser	Arg	Leu	Asn
															110
Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu	Asn	Leu	Ile	Leu
															125
His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	Asn	Asp	Ile	Ala
															140
Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro	Ser	Arg
															160
Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	Asn	Asp	Pro	Gln	Phe
															175
Gly	Thr	Ser	Cys	Glu	Ile	Thr	Gly	Phe	Gly	Lys	Glu	Asn	Ser	Thr	Asp
															190
Tyr	Leu	Tyr	Pro	Glu	Gln	Leu	Lys	Met	Thr	Val	Val	Lys	Leu	Ile	Ser
															205
His	Arg	Glu	Cys	Gln	Gln	Pro	His	Tyr	Tyr	Gly	Ser	Glu	Val	Thr	Thr
															220
Lys	Met	Leu	Cys	Ala	Ala	Asp	Pro	Gln	Trp	Lys	Thr	Asp	Ser	Cys	Gln
															240
Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Ser	Leu	Gln	Gly	Arg	Met	Thr
															255
Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Arg	Gly	Cys	Ala	Leu	Lys	Asp	Lys
															270
Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser	His	Phe	Leu	Pro	Trp	Ile	Arg	Ser
															285
His	Thr	Lys	Glu	Gln	Asn	Gly	Leu	Ala	Leu	Phe	Pro	Ile	Pro	Leu	Pro
															300

Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile
305 310 315 320

Pro Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val
325 330 335

Pro Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser
340 345 350

Val Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val
355 360 365

Cys Arg Leu Val Leu Arg Cys Ser Met His His His His His His
370 375 380